



**Supplementary Figure 5.** Comparison of gene expression data obtained from real-time RT-PCR and microarray experiments. Gene expression in RT-PCR experiments was normalized to the expression level of *GAPDH* (*Gapdh*) in the sample, and gene expression ratios between HCC and normal liver was calculated from normalized values of gene expression. Four genes listed in Supplementary Table 1 are selected for experiments. (a) Expression levels of *ASK*, *GTSE1*, *SLC16A2*, and *INHBC* in each subclass of human HCC measured by microarray experiments. (b) Expression levels of *ASK*, *GTSE1*, *SLC16A2*, and *INHBC* in each subclass of human HCC measured by real-time RT-PCR experiments. (c) Expression levels of *Ask*, *Gtse1*, *Slc16a2*, and *Inhbc* in each group of mouse HCC measured by microarray experiments. (d) Expression levels of *Ask*, *Gtse1*, *Slc16a2*, and *Inhbc* in each group of mouse HCC measured by real-time RT-PCR experiments. The values are represented by mean+SE of gene expression for 7 HCC tissues (human) and 5 HCC tissues (mouse) from each group.